



Qy	61 NADNTNGHGHVAGVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 120	Qy	121 AGARIHTNSGAAVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 180
Qy	121 AGARIHTNSGAAVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 180	Qy	121 AGARIHTNSGAAVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 180
Db	121 AGARIHTNSGAAVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 180	Db	121 AGARIHTNSGAAVNGAYTDSRNVDYRKNDMTIIFAGNEGNGGTTISAPGAKNAI 180
Qy	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240	Qy	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240
Db	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240	Db	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240
Qy	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240	Qy	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240
Db	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240	Db	181 TVGATENLRPSGSYADNINHVAQFSRGPTKDRKPDNAPGFTILSRSLLAPDSSF 240
Qy	241 WANEDSKRAYMGGTSMATPIVAGNVAQLEHHVKGRTPKPSLLKAALAGAAIGLY 300	Qy	241 WANEDSKRAYMGGTSMATPIVAGNVAQLEHHVKGRTPKPSLLKAALAGAAIGLY 300
Db	241 WANEDSKRAYMGGTSMATPIVAGNVAQLEHHVKGRTPKPSLLKAALAGAAIGLY 300	Db	241 WANEDSKRAYMGGTSMATPIVAGNVAQLEHHVKGRTPKPSLLKAALAGAAIGLY 300
Qy	301 PGNQGNGRVTLDKSLNTAYNNESSLTSQKATSYSTTACKPLKICSLYSDAPASTA 360	Qy	301 PGNQGNGRVTLDKSLNTAYNNESSLTSQKATSYSTTACKPLKICSLYSDAPASTA 360
Db	301 PGNQGNGRVTLDKSLNTAYNNESSLTSQKATSYSTTACKPLKICSLYSDAPASTA 360	Db	301 PGNQGNGRVTLDKSLNTAYNNESSLTSQKATSYSTTACKPLKICSLYSDAPASTA 360
Qy	361 SYTLDVNDLNLVITAPNGTQYQGNDFTSPYNDNGRNVENVFINAPQSGTYTIEVQATN 420	Qy	361 SYTLDVNDLNLVITAPNGTQYQGNDFTSPYNDNGRNVENVFINAPQSGTYTIEVQATN 420
Db	361 SYTLDVNDLNLVITAPNGTQYQGNDFTSPYNDNGRNVENVFINAPQSGTYTIEVQATN 420	Db	361 SYTLDVNDLNLVITAPNGTQYQGNDFTSPYNDNGRNVENVFINAPQSGTYTIEVQATN 420
Qy	421 VPVGPQTFSLAIVN 434	Qy	421 VPVGPQTFSLAIVN 434
Db	421 VPVGPQTFSLAIVN 434	Db	421 VPVGPQTFSLAIVN 434
RESULT 3			
US-09-985-689A-2			
; Sequence 2, Application US/0985689A			
; Publication No. US0030023351A1			
; GENERAL INFORMATION:			
; APPLICANT: HATADA, YUJI			
; APPLICANT: OGAWA, AKINORI			
; APPLICANT: KAGEYAMA, YASUHI			
; APPLICANT: SATO, TSUYOSHI			
; APPLICANT: ARAKI, HIROYUKI			
; APPLICANT: SUMITOMO, NOBUYUKI			
; APPLICANT: OKUDA, MITSUYOSHI			
; APPLICANT: SAEKI, KATSUHIKO			
; TITLE OF INVENTION: Alkaline protease			
; FILE REFERENCE: 215481US0			
; FILE REFERENCE: 215481US0			
; CURRENT APPLICATION NUMBER: US/09/985, 689A			
; CURRENT FILING DATE: 2002-07-01			
; CURRENT APPLICATION NUMBER: JP P2000-155166			
; CURRENT FILING DATE: 2000-11-22			
; PRIOR APPLICATION NUMBER: JP P2001-114048			
; PRIOR FILING DATE: 2001-04-12			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO: 2			
; LENGTH: 434			
; TYPE: PRT			
; ORGANISM: Bacillus sp.			
US-09-985-689A-2			
Query Match 97.3%; Score 2186; DB 10; Length 434;			
Best Local Similarity 96.1%; Pred. No. 4e-18; 2; Indels 0; Gaps 0;			
Matches 418; Conservative 14; Ns matches 0;			
Qy 1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
;			
1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
;			
61 NADNTNGHGHVAGVNGSTNGKGMQANLIVFOSIMDSCGGJGLPSNLQLFSQYS 120			
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61 NADNTNGHGHVAGVNGSTNGKGMQANLIVFOSIMDSCGGJGLPSNLQLFSQYS 120			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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61 NADNTNGHGHVAGVNGSTNGKGMQANLIVFOSIMDSCGGJGLPSNLQLFSQYS 120			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
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1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
; ;			
1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
; ;			
1 NDVARGTIVKADVAQSSYGLYGGQQLVAVADGOLDGRNDSSMHEFRGKITALYALGRTN 60			
; ;			

QY 241 WNHDSKYA<sup>NGGT</sup>SMATPIVAGNYAQLREHFVORGITPKPSLKAALIAGAADIGLY 300  
 241 WNHDSKYA<sup>NGGT</sup>SMATPIVAGNYAQLREHFVORGITPKPSLKAALIAGAADIGLY 300  
 DB 301 PGNQGNGRVLTDLSLNVAYNESSSLSTQKATYSTTAKPLKISLWSDAPSTA 360  
 QY 301 PGNQGNGRVLTDLSLNVAYNESSSLSTQKATYSTTAKPLKISLWSDAPSTA 360  
 DB 301 PGNQGNGRVLTDLSLNVAYNESSSLSTQKATYSTTAKPLKISLWSDAPSTA 360  
 QY 361 SVTLVNDLNLTAPNGTQYNGDFTSPYNDWGRNVENTFINAQSGTYTIEVQAIN 420  
 DB 361 SVTLVNDLNLTAPNGTQYNGDFTSPYNDWGRNVENTFINAQSGTYTIEVQAIN 420  
 QY 421 VPVGPQTESLAIVN 434  
 DB 421 VPVGPQTESLAIVN 434  
 DB 421 VPVGPQAFSLAIVN 434

RESULT 5

US-09-985-689A-7

; Sequence 7, Application US/09985689A  
 ; Publication No. US20030022351A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HATADA, YUJI  
 ; APPLICANT: OGAWA, AKINORI  
 ; APPLICANT: KAGEYAMA, YASUSHI  
 ; APPLICANT: SATO, TSUYOSHI  
 ; APPLICANT: ARAKI, HIROYUKI  
 ; APPLICANT: SUMITOMO, NOBUYUKI  
 ; APPLICANT: OKUDA, MITSUOSHI  
 ; APPLICANT: SAEKI, KATSUHISA  
 ; TITLE OF INVENTION: Alkaline proteases  
 ; FILE REFERENCE: 215:831US0  
 ; CURRENT APPLICATION NUMBER: US/09/985, 689A  
 ; CURRENT FILING DATE: 2002-07-01  
 ; PRIORITY NUMBER: JP P2000-355166  
 ; PRIORITY FILING DATE: 2000-11-22  
 ; PRIORITY APPLICATION NUMBER: JP P2001-114048  
 ; PRIORITY FILING DATE: 2001-04-12  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO: 7  
 ; LENGTH: 433  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 US-09-985-689A-7

Query Match 94.4% Score 2120.5; DB 10; Length 433;  
 Best Local Similarity 93.3%; Pred. No. 2.1e-176;  
 Matches 405; Conservative 20; Mismatches 8; Indels 1; Gaps 1;

QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60  
 DB 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60  
 QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60  
 DB 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60

Query Match 95.1% Score 2138; DB 10; Length 434;  
 Best Local Similarity 93.3%; Pred. No. 6.2e-178;  
 Matches 405; Conservative 20; Mismatches 9; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60  
 DB 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60  
 QY 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 180  
 DB 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 179  
 QY 61 NANDPQGHGTHVAGSVLGNSTNGKMAPANLYFQSIMDGGGLPSNLQTLFSQAYS 120  
 DB 61 NANDPQGHGTHVAGSVLGNSTNGKMAPANLYFQSIMDGGGLPSNLQTLFSQAYS 120  
 QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 240  
 DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 239  
 QY 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 180  
 DB 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 180  
 QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 240  
 DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 240  
 QY 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 180  
 DB 121 AGARIHTNSWGAAYNGAYTIDSRNVDYDVRNDMILFAGNREGPNGGTISAPGTAKNAI 180  
 QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 240  
 DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDRGKPYDAPTEFLSARSSLAPDSSF 240  
 QY 241 WNHDSKYA<sup>NGGT</sup>SMATPIVAGNYAQLREHFVORGITPKPSLKAALIAGAADIGLY 300  
 DB 241 WNHDSKYA<sup>NGGT</sup>SMATPIVAGNYAQLREHFVORGITPKPSLKAALIAGAADIGLY 300  
 QY 301 PGNQGNGRVLTDLSLNVAYNESSSLSTQKATYSTTAKPLKISLWSDAPSTA 360  
 DB 301 PGNQGNGRVLTDLSLNVAYNESSSLSTQKATYSTTAKPLKISLWSDAPSTA 360  
 QY 361 SVTLVNDLNLTAPNGTQYNGDFTSPYNDWGRNVENTFINAQSGTYTIEVQAIN 420  
 DB 360 SVTLVNDLNLTAPNGTQYNGDFTSPYNDWGRNVENTFINAQSGTYTIEVQAIN 419  
 QY 421 VPVGPQTESLAIVN 434



APPLICANT: SUMITOMO, NOBUYUKI  
 APPLICANT: OKUDA, MITSUYOSHI  
 APPLICANT: SAEKI, KATSUHISA  
 TITLE OF INVENTION: Alkaline proteases  
 CURRENT APPLICATION NUMBER: US/09/985,689A  
 CURRENT FILING DATE: 2002-07-01  
 PRIORITY NUMBER: JP P2000-355166  
 PRIOR FILING DATE: 2000-11-22  
 PRIORITY NUMBER: JP P2001-114048  
 PRIOR FILING DATE: 2001-04-12  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO: 4  
 LENGTH: 433  
 TYPE: PRT  
 ORGANISM: *Bacillus* sp.  
 US-09-985-689A-4

Query Match 88.2%; Score 1982.5; DB 10; Length 433;  
 Best Local Similarity 87.1%; Pred. No. 2.3e-164; Indels 1; Gaps 1;  
 Matches 378; Conservative 30; Mismatches 10; Gaps 1;

Qy 1 NDVARGIVKADAVQSSYGLGGQIVTAVALDTGLDGRNDSSMHEAFRGKITAYALGRTN 60  
 Db 1 NDVARGIVKADAVQNNYGLGGQIVTAVALDTGLDGRNDSSMHEAFRGKITAYALGRTN 60  
 Qy 61 NANDTNGHGHYAGSVLNGSTNKGMAPOANLYFOSIMDGGGCOLPSNQTLFSQAYS 120  
 Db 61 NASDPNGHGHGHYAGSVLNGSTNKGMAPOANLYFOSIMDGGGCOLPSNQTLFSQASN 119  
 Qy 121 AGARITHNSWGAVVNGAYTDSRNVDYDVRNDMTILFAAGNEGPNGTISAPGTAKNAI 180  
 Db 121 AGARITHNSWGAVVNGAYTDSRNVDYDVRNDMTILFAAGNEGPNGTISAPGTAKNAI 180  
 Qy 148 AGARITHNSWGAVVNGAYTDSRNVDYDVRNDMTILFAAGNEGPNGTISAPGTAKNAI 207  
 Db 148 AGARITHNSWGAVVNGAYTDSRNVDYDVRNDMTILFAAGNEGPNGTISAPGTAKNAI 207

Query Match 88.2%; Score 1982.5; DB 10; Length 433;  
 Best Local Similarity 87.1%; Pred. No. 2.3e-164; Indels 1; Gaps 1;  
 Matches 378; Conservative 30; Mismatches 10; Gaps 1;

Qy 181 TVGATENLRPSFGSYAQNINHYAQFSRGPPDGRKPDWAPGFTLSASSLADSSF 240  
 Db 208 TVGATENLRPSFGSYAQNINHYAQFSRGPPDGRKPDWAPGFTLSASSLADSSF 267  
 Qy 241 WANEDSKTAYMGTSMATPIAVGNVACOLREHTVKRKT1PKPSLILKALINGAABDGLGY 300  
 Db 268 WANEDSKTAYMGTSMATPIAVGNVACOLREHTVKRKT1PKPSLILKALINGAABDGLGY 327

RESULT 10  
 US-10-403-105-13  
 Sequence 13; Application US/10403105  
 Publication No. US20030180933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Hansen, Peter K.  
 ; APPLICANT: Bauditz, Peter K.  
 ; APPLICANT: Mikkelsen, Frank  
 ; TITLE OF INVENTION: Protease Variants And Compositions  
 ; FILE REFERENCE: 5435-200-US  
 ; CURRENT APPLICATION NUMBER: US/10/403-105  
 ; CURRENT FILING DATE: 2003-03-31  
 ; PRIOR APPLICATION NUMBER: US/09/196,281A  
 ; PRIOR FILING DATE: 1998-11-19  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-21  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO: 13  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: *Bacillus* sp.  
 US-10-403-105-13

Query Match 70.4%; Score 1581.5; DB 14; Length 345;  
 Best Local Similarity 95.3%; Pred. No. 1.7e-129; Indels 1; Gaps 1;  
 Matches 303; Conservative 10; Mismatches 4; Gaps 1;

Qy 1 NDVARGIVKADAVQSSYGLGGQIVTAVALDTGLDGRNDSSMHEAFRGKITAYALGRTN 60  
 Db 29 NDVARGIVKADAVQNNYGLGGQIVTAVALDTGLDGRNDSSMHEAFRGKITAYALGRTN 88  
 Qy 61 NANDTNGHGHYAGSVLNGSTNKGMAPOANLYFOSIMDGGGCOLPSNQTLFSQAYS 120  
 Db 89 NANDTNGHGHYAGSVLNGSTNKGMAPOANLYFOSIMDGGGCOLPSNQTLFSQAYS 147  
 Qy 121 AGARITHNSWGAVVNGAYTDSRNVDYDVRNDMTILFAAGNEGPNGTISAPGTAKNAI 180

Db 148 AGARIHTNSWGA~~YNGAYT~~TD~~SRY~~ND~~MTL~~FFAGNE~~GPGS~~CTISAPG~~TAKNAI~~ 207  
 Qy 181 T~~GATENL~~RS~~FGS~~YAD~~DNHVA~~Q~~SSR~~GT~~KDRIK~~P~~DMAP~~TF~~IL~~AS~~SLA~~PD~~SF~~ 240  
 Db 208 T~~GATENL~~RS~~FGS~~YAD~~DNHVA~~Q~~SSR~~GT~~KDRIK~~P~~DMAP~~TF~~IL~~AS~~SLA~~PD~~SF~~ 267

RESULT 12  
 US-10-090-624-1  
 Sequence 1, Application US/10090624  
 Publication No. US2002013235A1  
 GENERAL INFORMATION:  
 APPLICANT: TAKAKURA, Hikaru  
 MORISHITA, Mio  
 SHIMOTO, Tomoko  
 ASADA, Kiyozo  
 APPLICANT: KATO, Iku~~noshin~~  
 TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE  
 FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 09/445,472  
 PRIORITY FILING DATE: 1999-12-06  
 NUMBER OF SEQ ID NOS: 33  
 SEQ ID NO: 12  
 LENGTH: 659  
 TYPE: PRT  
 ORGANISM: Thermococcus celer  
 US-10-090-624-12

Query Match 19.9%; Score 447 5; DB 13; Length 659;  
 Best Local Similarity 29.8%; Pred. No. 4e-30;  
 Matches 137; Conservative 68; Mismatches 153; Indels 101; Gaps 18;

Qy 8 V~~KADVA~~QSS~~Y~~GG~~O~~IV~~A~~V~~A~~D~~G~~T~~G~~R~~D~~S~~M~~Y~~H~~EA~~F~~R~~K~~IT~~Y~~-~~A~~l~~G~~R~~T~~N~~N~~AN~~D~~T~~N~~ 66  
 Db 145 I~~G~~A~~D~~T~~V~~N~~S~~L~~G~~D~~G~~S~~G~~V~~R~~V~~A~~V~~I~~D~~G~~D~~A~~N~~---~~HP~~D~~L~~G~~K~~V~~W~~Y~~D~~A~~V~~G~~R~~T~~P~~Y~~D~~O~~ 198  
 Qy 67 G~~H~~G~~T~~H~~V~~A~~G~~S~~V~~L~~G~~S~~T~~N~~K~~-~~G~~MA~~P~~Q~~A~~N~~L~~V~~Q~~FS~~I~~M-~~D~~SG~~G~~GL~~G~~L~~P~~S~~N~~Q~~T~~L~~S~~Q~~A~~Y~~S~~A~~1~~ 121  
 Db 199 G~~H~~G~~T~~H~~V~~A~~G~~I~~V~~A~~G~~T~~G~~S~~N~~S~~Q~~Y~~V~~G~~A~~P~~G~~K~~V~~K~~G~~D~~G~~S~~S~~V~~T~~I~~G~~D~~W~~V~~Y~~Q~~N~~K~~D~~X~~2~~ 258  
 Qy 122 G~~A~~R~~I~~-~~---~~H~~T~~N~~S~~W~~A~~Y~~G~~A~~T~~Y~~T~~D~~S~~R~~N~~Y~~D~~Y~~R~~K~~D~~M~~T~~L~~F~~A~~G~~N~~E~~G~~P~~G~~G~~ 169  
 Db 259 G~~I~~R~~V~~I~~N~~S~~L~~G~~S~~S~~O~~S~~D~~G~~D~~S~~L~~S~~Q~~Y~~A~~N~~N~~S~~C~~P~~N~~T~~Y~~ 306  
 Qy 170 I~~S~~A~~P~~G~~T~~A~~R~~N~~A~~T~~Y~~G~~A~~T~~N~~L~~R~~P~~S~~G~~T~~A~~D~~N~~I~~N~~H~~A~~V~~Q~~F~~S~~R~~G~~T~~K~~D~~R~~K~~P~~D~~M~~A~~P~~F~~L~~S~~ 229  
 Db 307 V~~G~~S~~P~~A~~A~~S~~K~~V~~I~~T~~G~~A~~---~~-~~V~~D~~S~~N~~D~~N~~I~~A~~S~~S~~R~~G~~T~~A~~D~~G~~R~~K~~P~~V~~E~~V~~A~~P~~G~~D~~I~~T~~A~~ 355  
 Qy 230 A~~R~~S~~S~~L~~A~~P~~S~~F~~W~~A~~N~~H~~D~~S~~K~~Y~~A~~Y~~M~~G~~G~~T~~S~~M~~A~~T~~P~~I~~V~~A~~G~~-~~N~~V~~A~~Q~~R~~E~~H~~F~~V~~R~~N~~R~~G~~I~~T~~P~~K~~-~~P~~S~~L~~X~~2~~ 286  
 Db 356 P~~R~~A~~S~~-~~G~~T~~S~~M~~G~~T~~P~~I~~D~~Y~~T~~K~~A~~S~~G~~T~~S~~M~~A~~T~~P~~H~~S~~G~~C~~A~~L~~O~~A~~H~~---~~-~~P~~S~~W~~T~~P~~D~~K~~T~~4~~ 404  
 Qy 287 A~~A~~L~~T~~A~~G~~A~~---~~-~~A~~G~~I~~G~~L~~P~~G~~N~~G~~Q~~G~~R~~V~~T~~D~~K~~S~~L~~---~~-~~N~~V~~A~~Y~~N~~E~~S~~S~~L~~S~~T~~E~~Q~~K~~A~~Y~~3~~ 335  
 Db 405 T~~F~~D~~V~~S~~G~~A~~F~~V~~T~~A~~T~~Y~~W~~~~---~~-~~G~~R~~N~~V~~A~~K~~Y~~D~~Y~~A~~T~~F~~G~~V~~A~~D~~K~~G~~S~~A~~5~~ 457  
 Qy 336 S~~F~~P~~T~~A~~G~~K~~P~~L~~K~~I~~S~~L~~V~~W~~D~~A~~P~~S~~T~~A~~T~~Y~~W~~D~~---~~-~~T~~G~~S~~D~~I~~D~~Y~~P~~G~~N~~E~~-~~V~~D~~S~~T~~Y~~A~~Y~~~~5~~ 500  
 Db 458 T~~F~~D~~V~~S~~G~~A~~F~~V~~T~~A~~T~~Y~~W~~~~---~~-~~T~~G~~S~~D~~I~~D~~Y~~P~~G~~N~~E~~-~~V~~D~~S~~T~~Y~~A~~Y~~~~5~~ 500

Qy 396 R~~N~~N~~V~~E~~N~~V~~F~~A~~N~~A~~P~~S~~G~~T~~Y~~I~~E~~Y~~Q~~A~~N~~V~~P~~G~~F~~Q~~T~~E~~S~~L~~A~~I~~V~~N~~4~~ 434  
 Db 501 -~~G~~F~~E~~V~~G~~Y~~N~~P~~T~~A~~T~~Y~~W~~T~~V~~K~~V~~S~~K~~-~~G~~R~~N~~V~~A~~Y~~Q~~D~~V~~V~~S~~ 534

RESULT 13  
 US-10-090-624-4  
 Sequence 4, Application US/10090624  
 Publication No. US2002013235A1  
 GENERAL INFORMATION:

RESULT 14  
 US-10-090-624-16  
 ; Sequence 16, Application US/10090624  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TAKAKURA, Hikaru  
 ; APPLICANT: MORISHITA, Mio  
 ; APPLICANT: SHIMOJO, Tomoko  
 ; APPLICANT: ASADA, Kiyozo  
 ; APPLICANT: KATO, Irunoshin  
 ; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE  
 ; FILE REFERENCE: TAKAKURA-6  
 ; CURRENT APPLICATION NUMBER: US/10/090, 624  
 ; PRIORITY FILING DATE: 1999-12-06  
 ; PRIORITY FILING DATE: 1997-06-10  
 ; PRIORITY FILING DATE: 1997-06-10  
 ; PRIORITY FILING DATE: 1999-12-06  
 ; PRIORITY FILING DATE: 1997-06-10  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 522  
 ; ORGANISM: Pyrococcus furiosus  
 ; FEATURE: misc\_feature  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (428)..(428)  
 ; OTHER INFORMATION: Xaa at position 428 is Gly or Val.  
 US-10-090-624-4

Query Match 18.2%; Score 409; DB 13; Length 522;  
 Best Local Similarity 29.6%; Pred. No. 6.6e-7;  
 Matches 135; Conservative 60; Mismatches 147; Indels 114; Gaps 19;

Qy 18 GLYGGGGIVAVADTGLDTGRNDSSMHEAFRKITIYALAGRNNN-----DTNGHGT 71  
 Db 22 GYDGSGTTGIDIDGID-----ASHPDLOQKV-----IGWVDFYNGRSVYDDHGT 202

Qy 72 VAGSVLNGSTN----KGMAPOANLYFQSIM-----PSNQTLFQAYSAGARI 125  
 Db 203 VASIAAGTGAAASNGKYGMAKGAKLAGIKVULGADGSSSISTIKGVWAVDNKDQYGIKV 262

Qy 126 HTNSWGA-----AVNGAYTDSRNDYDTRKNDMILFAGNEGNGGTIS 173  
 Db 263 INSLGSSSDDTDAUSQAVNAAWDA-----GLVWVAGNSGPNKYTTGSP 310

Qy 174 GTAKNAITYGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDTMAPGTFILSARS 233  
 Db 311 AAASKVITYGA-----VDKYDITTSFSSRGTADEGRKPEVAPRNWIIARAS 359

Qy 234 LAPDSSEWANHDSSKAYANGTGTSMATPVAGNVAQLRHFTVNRGTPK-PSLKLALIA 291  
 Db 360 --GTSMGQCPINDYYTAAPGTSMATPVAGIAILLQ-----AHSWTPDVKPZLIA 409

Qy 292 GA-----ADIGLGYPNQNGWGRYTLDKSLNVAYNNESSSLSTSQKA-----TYSFT 338  
 Db 410 TADIVKPDDEIADAYGA-----GRVNAKAIN-1DNYAKLVLFTSYVANKGSQTHQFV 460

Qy 174 GTAKNAITYGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDTMAPGTFILSARS 233  
 Db 179 AAASKVITYGA-----VDKYDITTSFSSRGTADEGRKPEVAPRNWIIARAS 227

Qy 234 LAPDSSEWANHDSSKAYANGTGTSMATPVAGNVAQLRHFTVNRGTPK-PSLKLALIA 291  
 Db 228 --GTSMGQCPINDYYTAAPGTSMATPVAGIAILLQ-----AHSWTPDVKTALIE 277

Qy 292 GA-----ADIGLGYPNQNGWGRYTLDKSLNVAYNNESSSLSTSQKA-----TYSFT 338  
 Db 399 VENYFINAQSGTYTIEQAYNNPVPGFOTSLAIVN 434

Qy 278 TADIVKPDDEIADAYGA-----GRVNAKAIN-1DNYAKLVLFTSYVANKGSQTHQFV 328

Qy 339 ATAGKPLKISLVSDDAPASSTAVLYNDLNIVITAPNGTQVGNFDTSPYNDNGRNN 398  
 Db 329 ISGASFVTTLYNDNAN-----SDLDLYDPMQ-VDYSTAY-----G 369

Qy 399 VENYFINAQSGTYTIEQAYNNPVPGFOTSLAIVN 434  
 Db 370 FEKVGYNPTDGTWIKVVS--GSANYQVDVVS 402

RESULT 15  
 US-10-112-488-39  
 ; Sequence 39, Application US/10112488  
 ; Publication No. US2003010082746A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIKUCHI, Yoshi-umi  
 ; APPLICANT: DATE, Masayo  
 ; APPLICANT: UMEIWA, Yukiko  
 ; APPLICANT: MATSU, Hiroshi  
 ; FILE REFERENCE: 219246US0007  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIORITY FILING DATE: 2000-09-29  
 ; PRIORITY FILING DATE: 2000-06-28  
 ; PRIORITY FILING DATE: 1999-09-30  
 ; PRIORITY FILING DATE: 1999-09-30  
 ; NUMBER OF SEQ ID NOS: 70

Query Match 18.2%; Score 409; DB 13; Length 654;  
 Best Local Similarity 29.6%; Pred. No. 9.1e-7;  
 Matches 135; Conservative 60; Mismatches 147; Indels 114; Gaps 19;

Qy 18 GLYGGGGIVAVADTGLDTGRNDSSMHEAFRKITIYALAGRNNN-----DTNGHGT 71  
 Db 154 GYDGSGTTGIDIDGID-----ASHPDLOQKV-----IGWVDFYNGRSVYDDHGT 202

Qy 72 VAGSVLNGSTN----KGMAPOANLYFQSIM-----PSNQTLFQAYSAGARI 125  
 Db 203 VASIAAGTGAAASNGKYGMAKGAKLAGIKVULGADGSSSISTIKGVWAVDNKDQYGIKV 262

Qy 126 HTNSWGA-----AVNGAYTDSRNDYDTRKNDMILFAGNEGNGGTIS 173  
 Db 263 INSLGSSSDDTDAUSQAVNAAWDA-----GLVWVAGNSGPNKYTTGSP 310

Qy 174 GTAKNAITYGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDTMAPGTFILSARS 233  
 Db 311 AAASKVITYGA-----VDKYDITTSFSSRGTADEGRKPEVAPRNWIIARAS 359

Qy 234 LAPDSSEWANHDSSKAYANGTGTSMATPVAGNVAQLRHFTVNRGTPK-PSLKLALIA 291  
 Db 360 --GTSMGQCPINDYYTAAPGTSMATPVAGIAILLQ-----AHSWTPDVKPZLIA 409

Qy 292 GA-----ADIGLGYPNQNGWGRYTLDKSLNVAYNNESSSLSTSQKA-----TYSFT 338  
 Db 410 TADIVKPDDEIADAYGA-----GRVNAKAIN-1DNYAKLVLFTSYVANKGSQTHQFV 460

Qy 174 GTAKNAITYGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDTMAPGTFILSARS 233  
 Db 179 AAASKVITYGA-----VDKYDITTSFSSRGTADEGRKPEVAPRNWIIARAS 227

Qy 234 LAPDSSEWANHDSSKAYANGTGTSMATPVAGNVAQLRHFTVNRGTPK-PSLKLALIA 291  
 Db 228 --GTSMGQCPINDYYTAAPGTSMATPVAGIAILLQ-----AHSWTPDVKTALIE 277

Qy 292 GA-----ADIGLGYPNQNGWGRYTLDKSLNVAYNNESSSLSTSQKA-----TYSFT 338  
 Db 399 VENYFINAQSGTYTIEQAYNNPVPGFOTSLAIVN 434

Qy 278 TADIVKPDDEIADAYGA-----GRVNAKAIN-1DNYAKLVLFTSYVANKGSQTHQFV 328

Qy 339 ATAGKPLKISLVSDDAPASSTAVLYNDLNIVITAPNGTQVGNFDTSPYNDNGRNN 398  
 Db 329 ISGASFVTTLYNDNAN-----SDLDLYDPMQ-VDYSTAY-----G 369

Qy 399 VENYFINAQSGTYTIEQAYNNPVPGFOTSLAIVN 434  
 Db 370 FEKVGYNPTDGTWIKVVS--GSANYQVDVVS 402

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1079
; TYPE: PRF
; ORGANISM: Streptomyces albogriseolus
US-112-488-39

Query Match Score 366; DB 14; Length 1079;
Best Local Similarity 31.6%; Pred No. 1.1e-22;
Matches 148; Conservative 55; Mismatches 175; Indels 90; Gaps 20;
3 VAR ---GIVKADVAQS-----SYGLYCGQQTIVAVADTGLDTCRNDSSMHEAFRG 48
Db 160 VARYWLDGVRKASIDTSVSGQITPRAWEAGYDGKVKAVLDFGVD----ATHPDLKG 213

Query 49 KITALYALGRTNNNANDTNGHTHAGSVLNGS ---TKKGMAPOQANIVFQ51MDSGGL 104
Db 214 QVTASKNFTSAPTTEDVVGHTHAYASIAAGTGAOSKGTYKVGAKILNGKVLDAG- 271

Query 105 GGLPSNLQITLESQAYSAGRAHINTNSWGAAVNGAYTDSRNVDDYVRK--NDMTLFF--AA 160
Db 272 FGDDSCILAGNEAAQGDIVNMSLG---GMDTPETPPLAEDVQLSAEKGILPATA 327

Query 161 GNEGPNGGTISAPGTAKNATIVGATENLPSFGSYADNTNHYAQFSSRGP-TKDGRKPD 219
Db 328 GNEGPQ--SIGSPGSDASDALTGA-----VDDDKLADFSSTCPRLDGAVKPD 374

Query 220 VMAPGFIILSSRSSLAPDSSWANHDSKAYMGGTISMAPIVAGNVAOREHHVRNGIT 279
Db 375 LTAPGVDITAAASAKNDIAKEVGKPGMTISGTSMAPPHVAGAAALKQQHPE---- 429

Query 280 PKPSLIIKAALIAGAADIGLG-YPNENQGNGRTVLDKSLNAYNESSSS----- 328
Db 430 WKYAEIUGALTASTKD--GKYPPEQGSSRVQVDTKATQTVIREPVSLSPGQWPHD 486

Query 329 ---TSOKATYSTFTATAGPKLKLISLWSD----APAS--TTASVTLVNDNLVITAP-NG 377
Db 487 DKPVTKLTYRNLTGTDVTLKLTSATGPKGKAAPAGFTLGAStL-----TVPANG 538

Query 378 TOXVGNDPITSYNDNDGRNVENTFINAQ-----GTYTLEQAYNV 421
Db 539 TASVDVTADTRLGAVDGTYSAYYATGAGOSVRTAAGVREVESYNV 586

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Search completed: March 18, 2004, 04:12:40  
 Job time : 47 secs



RESULT 2  
 US-10-385-662-2  
 ; Sequence 2, Application US/10385662  
 ; Publication No. US2004000432A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OKUDA, MITSUYOSHI  
 ; APPLICANT: SATO, TSUYOSHI  
 ; APPLICANT: Saito, Kazuhiro  
 ; APPLICANT: SUMITOMO, NOBUYUKI  
 ; APPLICANT: IZAWA, YOSHIFUMI  
 ; APPLICANT: SAEKI, KATSURISA  
 ; APPLICANT: KOBAYASHI, TOHRU  
 ; APPLICANT: NOMURA, MASAFUMI  
 ; TITLE OF INVENTION: Alkaline protease  
 ; FILE REFERENCE: 231938US0  
 ; CURRENT APPLICATION NUMBER: US/10/385,662  
 ; CURRENT FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: JP 2002-081428  
 ; PRIOR FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: JP 2002-165947  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: JP 2002-304231  
 ; PRIOR FILING DATE: 2002-10-06  
 ; SEQ ID NO: 2  
 ; LENGTH: 434  
 ; TYPE: PRT  
 ; ORGANISM: *Bacillus* sp. KSM-KP43  
 ; NUMBER OF SEQ ID NOs: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 434  
 ; Query Match: 99.8%; Score: 2242; DB: 15; Length: 434;  
 ; Best Local Similarity: 99.8%; Pred. No: 5.2e-18;  
 ; Matches: 433; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;  
 ; US-10-385-662-2

RESULT 3  
 US-10-985-689A-2  
 ; Sequence 2, Application US/09985689A  
 ; Publication No. US20030022351A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HATADA, YUJI  
 ; APPLICANT: OGAWA, AKINORI  
 ; APPLICANT: KAGEYAMA, YASUSHI  
 ; APPLICANT: SATO, TSUYOSHI  
 ; APPLICANT: ARAKI, HIROYUKI  
 ; APPLICANT: SUMITOMO, NOBUYUKI  
 ; APPLICANT: OKUDA, MITSUYOSHI  
 ; APPLICANT: SAEKI, KATSURISA  
 ; TITLE OF INVENTION: Alkaline proteases  
 ; FILE REFERENCE: 215483US0  
 ; CURRENT APPLICATION NUMBER: US/09/985,689A  
 ; CURRENT FILING DATE: 2002-07-01  
 ; PRIOR APPLICATION NUMBER: JP P2000-355166  
 ; PRIOR FILING DATE: 2000-11-22  
 ; PRIOR APPLICATION NUMBER: JP P2001-114048  
 ; PRIOR FILING DATE: 2001-04-12  
 ; NUMBER OF SEQ ID NOs: 7  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 434  
 ; TYPE: PRT  
 ; ORGANISM: *Bacillus* sp.  
 ; US-09-985-689A-2

Query Match: 97.3%; Score: 2186; DB: 10; Length: 434;  
 ; Best Local Similarity: 96.3%; Pred. No: 4e-182;  
 ; Matches: 418; Conservative: 14; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 NDVARGIVRADVAQSYGLYGOGIVAVADTGIDTGRNDSSMHEFRGKITALYALGRTN 60  
 Db 1 NDVARGIVRADVAQSYGLYGOGIVAVADTGIDTGRNDSSMHEFRGKITALYALGRTN 60

QY 61 NANDTNGHGHGTHVAGVNGAYTDSRNDYDVRNDMFTKGRDSSMHEFRGKITALYALGRTN 120  
 Db 61 NANDTNGHGHGTHVAGVNGAYTDSRNDYDVRNDMFTKGRDSSMHEFRGKITALYALGRTN 120

QY 121 AGARITHNSWGAAGVNGAYTDSRNDYDVRNDMFTKGRDSSMHEFRGKITALYALGRTN 180  
 Db 121 AGARITHNSWGAAGVNGAYTDSRNDYDVRNDMFTKGRDSSMHEFRGKITALYALGRTN 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPKDKRIPDKDGR1KPDYMAPGTFILSARSSLAPDSSF 240  
 Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPKDKRIPDKDGR1KPDYMAPGTFILSARSSLAPDSSF 240

QY 241 WANHDSSKAYAMGGTSMAPTIVAGNYQLREHFVKGITPKPSLKAALJAGAAGDGLGY 300  
 Db 241 WANHDSSKAYAMGGTSMAPTIVAGNYQLREHFVKGITPKPSLKAALJAGAAGDGLGY 300

QY 301 PNGNQGWRVTLDKSLNVAYNESSLSTSQATYSFTATGPKLKLISLYWDAPASTTA 360  
 Db 301 PNGNQGWRVTLDKSLNVAYNESSLSTSQATYSFTATGPKLKLISLYWDAPASTTA 360

QY 361 SVTLVNDLNVITAPNGTQYVGNDFSPYNDNWDGNNVENVFIAPOSQSTYIEQAYN 420  
 Db 361 SVTLVNDLNVITAPNGTQYVGNDFSPYNDNWDGNNVENVFIAPOSQSTYIEQAYN 420

QY 421 VPVGPQTFSLAVN 434  
 Db 421 VPVGPQTFSLAVN 434

Qy	241	WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNGITPKPSLKKALIAGADIGLY	300
Dib	241	WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNGITPKPSLKKALIAGADIGLY	300
Qy	301	PNGNQGWRVTLDSKLNVAYNNESSLSTSQATYSFTATAGKPKLKSILWNSDAPASTTA	360
Db	301	PNGNQGWRVTLDSKLNVAYNNESSLSTSQATYSFTATAGKPKLKSILWNSDAPASTTA	360
Qy	361	SYTLVNDLNLVITAPNGTQYNGNDFTSPYNDWGRNNVENTIFNAPSGTYTIEVQAYN	420
Db	361	SYTLVNDLNLVITAPNGTQYNGNDFTSPYNDWGRNNVENTIFNAPSGTYTIEVQAYN	420
Qy	421	VPVGQPQFESLAVN	434
Db	421	VPVGQPQFESLAVN	434
RESULT 4			
	US-09-985-689A-6		
	Sequence 6: Application US/09985689A		
	Publication No. US20030022351A1		
	GENERAL INFORMATION:		
	APPLICANT: HATADA, YUJI		
	APPLICANT: OGAWA, AKINORI		
	APPLICANT: KAGEYAMA, YASUHI		
	APPLICANT: SATO, TSUYOSHI		
	APPLICANT: ARAKI, HIROYUKI		
	APPLICANT: SUMITOMO, NOBUYUKI		
	APPLICANT: OKUDA, MITSUYOSHI		
	APPLICANT: SAEKI, KATSUOSA		
	TITLE OF INVENTION: Alkaline proteases		
	FILE REFERENCE: 215-83050		
	CURRENT APPLICATION NUMBER: US/09/985,689A		
	CURRENT FILING DATE: 2002-07-01		
	PRIOR APPLICATION NUMBER: JP P2000-355166		
	PRIOR FILING DATE: 2000-11-22		
	PRIOR APPLICATION NUMBER: JP P2001-114048		
	PRIOR FILING DATE: 2001-04-12		
	NUMBER OF SEQ ID NOS: 7		
	SOFTWARE: PatentIn version 3.1		
	SEQ ID NO 6		
	LENGTH: 434		
	TYPE: PRT		
	ORGANISM: Bacillus sp.		
	US-09-985-689A-6		
Qy	1	NDVARGIVKADVAQSYGLYQGQVIVAVADTGLDTRGRNDSMMEFRGKITALYALGRTN	60
Db	1	NDVARGIVKADVAQSYGLYQGQVIVAVADTGLDTRGRNDSMMEFRGKITALYALGRTN	60
Qy	61	NANDNGHGHVAGSVLGNGSTNGKMAPQANLYFQSINDSGGGIIGGLPBNLQLTFSQAYS	120
Db	61	NANDNGHGHVAGSVLGNGSTNGKMAPQANLYFQSINDSGGGIIGGLPBNLQLTFSQAYS	120
Qy	121	AGARIHTNSWGAAYNGAYTDSRNIVDDYRKNDTILFAGNEQNGGTTISAPTKAKAI	180
Dib	121	AGARIHTNSWGAAYNGAYTDSRNIVDDYRKNDTILFAGNEQNGGTTISAPTKAKAI	180
Qy	181	TVGATENLRPSFGSYADNINHVAOFSSRGPTKDRKIPDVMAPGTFILSARSSAPDSSF	240
Db	181	TVGATENLRPSFGSYADNINHVAOFSSRGPTKDRKIPDVMAPGTFILSARSSAPDSSF	240
Qy	241	WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNGITPKPSLKKALIAGADIGLY	300
Db	241	WANHDSKYAYMGGTSMATPIVAGNVAOLREHFVNGITPKPSLKKALIAGADIGLY	300
Qy	301	PNGNQGWRVTLDSKLNVAYNNESSLSTSQATYSFTATAGKPKLKSILWNSDAPASTTA	360

Db	301	PSGNGQWGRVYTLDKSLNVAFNETSLSLNQKATYTSFTAQSCKPLKISLVSNDAPPSTA	3.60
Qy	3.61	SVTLVNDLNVLITVANGTOVYGVNDFTSPYNDWGRNNTENVNAPQSGTYTIEVQAYN	4.20
Db	3.61	SVTLVNDLNVLITVANGTOVYGVNDFTAPYDNWGRNNTENVNAPQSGTYTIEVQAYN	4.20
Qy	4.21	VPVGPOTESLAIVN	4.34
Db	4.21	VPQGQAFSLAIVN	4.34
RESULT 5			
	US-09-985-689A-7		
	Sequence 7, Application US/09985-689A		
	Publication No. US20040022351A1		
	GENERAL INFORMATION:		
	APPLICANT: HATAKE, YUJI		
	APPLICANT: OGAWA, AKINORI		
	APPLICANT: KAGAYAMA, YASUHI		
	APPLICANT: SATO, TSUYOSHI		
	APPLICANT: ARAKI, HIROYUKI		
	APPLICANT: SUMITOMO, NOBUYUKI		
	APPLICANT: OKUDA, MITSUYOSHI		
	APPLICANT: SAEKI, KATSUHISA		
	TITLE OF INVENTION: Alkaline proteases		
	FILE REFERENCE: 2154433US0		
	CURRENT APPLICATION NUMBER: US/09/985, 689A		
	CURRENT FILING DATE: 2004-07-01		
	PRIOR APPLICATION NUMBER: JP P2000-355166		
	PRIOR FILING DATE: 2000-11-22		
	PRIOR APPLICATION NUMBER: JP P2001-114048		
	NUMBER OF SEQ ID NOS: 7		
	SOFTWARE: Patentin version 3.1		
	SEQ ID NO 7		
	TYPE: PRT		
	ORGANISM: Bacillus sp.		
	US-09-985-689A-7		
	Query Match 94.4%; Score 2120.5; DB 10; Length 433;		
	Best Local Similarity 93.3%; Pred. No. 2.1e-176; Mismatches 8; Indels 1; Gaps 1;		
	Matches 405; Conservative 20; Missmatches 8;		
Qy	1 NDVARIGVADYQSSSYGLYQGQGVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN	60	
Db	1 NDVARIGVADYQSSSYGLYQGQGVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN	60	
Qy	61 NANDTNGHGTIVAGSYLGNQNSTNGKMAPQANLYFQSINDSGGGIIGGLPSNLQTLFSQAYS	120	
Db	61 NANDTNGHGTIVAGSYLGN-ATNKGKMAPQANLYFQSINDSGGGIIGGLPSNLQTLFSQAYS	119	
Qy	121 AGARHTTNSMAAVNGAYTDSRNTDLYPRNDMILFAGNNGPQNGTISAGTAKNAI	180	
Db	120 AGARHTTNSCAAVNGAYTDSRNTDLYPRNDMILFAGNNGPQNGTISAGTAKNAI	179	
Qy	181 TVGATENLRPFSYADNTNVAQFSSRGFTDKRJIKPDVMAPTFILSARSSLPDSSF	240	
Db	180 TVGATENLRPFSYADNTNVAQFSSRGFTDKRJIKPDVMAPTFILSARSSLPDSSF	239	
Qy	241 WANHDSKYATMGGTSMATPIVAGNYAQOLREHFYVNGTIPKPKPSLKAALIAGADIGLGY	300	
Db	240 WANHDSKYATMGGTSMATPIVAGNYAQOLREHFYVNGTIPKPKPSLKAALIAGADIGLGY	299	
Qy	301 PGNQGQWGRVYTLDKSLNVAFNETSQATAGKPLKISLVSNDAPPSTA	360	
Db	300 PGNQGQWGRVYTLDKSLNVAFNETSQATAGKPLKISLVSNDAPPSTA	359	
Qy	361 SVTLVNDLNVLITVANGTOVYGVNDFTSPYNDWGRNNTENVNAPQSGTYTIEVQAYN	4.20	
Db	360 SVTLVNDLNVLITVANGTOVYGVNDFTAPYDNWGRNNTENVNAPQSGTYTIEVQAYN	4.19	
Qy	421 VPVGPOTESLAIVN	4.34	



```

; SEQ ID NO: 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-10

Query Match 70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1; e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1; Gaps 1

Qy 1 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 60
Db 29 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 88
Db 61 NANTNGHCTHYAGSVLNGSTNGKMAQANLYFQSINDSGGGGFLSNLQTLFSAYS 120
Db 89 NANTNGHCTHYAGSVLGN-ATNGKMAQANLYFQS1MDSGGGGFLSPNQTLFSAYS 147
Db 121 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 180
Db 148 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 207
Db 181 TVGATENRPSFGSYADNINHYAQFSSRGPHDRGRKPDWAPGFTLSSASSLAPDSSF 240
Db 208 TVGATENRPSFGSYADNINHYAQFSSRGPHDRGRKPDWAPGFTLSSASSLAPDSSF 267
Db 241 WANFDKSIAYMGTSMATPIVAGNAVLQREHFVKGITPKESLKLAKLINGAAAGLGY 300
Db 268 WANFDKSIAYMGTSMATPIVAGNAVLQREHFVKGITPKESLKLAKLINGAAAGLGY 327
Db 301 PNGNQGRVTLDSKLV 318
Db 328 PNGNQGRVTLDSKLV 345
Db 360 PNGNQGRVTLDSKLV 345

RESULT 10
US-10-403-105-13
Query Match 70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1; e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1; Gaps 1

Qy 1 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 60
Db 1 NANTNGHCTHYAGSVLNGSTNGKMAQANLYFQSINDSGGGFLSPNQTLFSAYS 120
Db 61 NANTNGHCTHYAGSVLNG-ATNGKMAQANLYFQS1MDSGGGFLSPNQTLFSAYS 119
Db 121 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 180
Db 120 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 179
Db 181 TVGATENRPSFGSYADNINHYAQFSSRGPHDRGRKPDWAPGFTLSSASSLAPDSSF 240
Db 180 TVGATENRPSFGSYADNINHYAQFSSRGPHDRGRKPDWAPGFTLSSASSLAPDSSF 239
Db 241 WANFDKSIAYMGTSMATPIVAGNAVLQREHFVKGITPKESLKLAKLINGAAAGLGY 300
Db 240 WANFDKSIAYMGTSMATPIVAGNAVLQREHFVKGITPKESLKLAKLINGAAAGLGY 299
Db 301 PNGNQGRVTLDSKLV 318
Db 300 PNDQDQGRVTLDSKLV 345
Db 361 SYLVNLNDLNLTATPNTQYVENDFTSPYNDGRNINVNTYFNAPOSCTYIEVQAYN 420
Db 360 SYLVNLNDLNLTATPNTQYVENDFTSPYNDGRNINVNTYFNAPOSCTYIEVQAYN 419
Db 421 VPYGPOTSLAIVN 434
Db 420 VPSGPQRFSLAIVN 433

RESULT 9
US-10-336-324-10
Query Match 70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1; e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1; Gaps 1

Qy 1 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 60
Db 29 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 88
Db 61 NANTNGHCTHYAGSVLNGSTNGKMAQANLYFQSINDSGGGFLSPNQTLFSAYS 120
Db 89 NANTNGHCTHYAGSVLGN-ATNGKMAQANLYFQS1MDSGGGFLSPNQTLFSAYS 147
Db 121 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 180

; SEQ ID NO: 11
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-10-403-105-13

Query Match 70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1; e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1; Gaps 1

Qy 1 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 60
Db 29 NDVARGIVADQSSYLYGQQIVAVADTGKDTGRNDSSMHEAFRKITAYALGRTN 88
Db 61 NANTNGHCTHYAGSVLNGSTNGKMAQANLYFQSINDSGGGFLSPNQTLFSAYS 120
Db 89 NANTNGHCTHYAGSVLGN-ATNGKMAQANLYFQS1MDSGGGFLSPNQTLFSAYS 147
Db 121 AGARHTNNGAANGAYTDSRNDDYVKNMDTILFAGNEGGNGTISAPGTAKNAI 180

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 39
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Streptomyces albogriseolus
; US-10-1112-488-39

Query Match 16.3%; Score 366; DB 14; Length 1079;
Best Local Similarity 31.8%; Pred. No. 1..1e-22;
Matches 148; Conservative 55; Mismatches 175; Indels 90; Gaps 20;

Qy 3 VAR---GIVKADVAQS-----SYGLYGGGIVAVADTGLDTGRNDTSSMEAFRG 48
Db 160 VARVNLGVKRAASLDTSVGQIQTPKAWEAGDKGKVIAVLDGIVD-----ATHFDLKG 213
Qy 49 KITALVALGRNNNANTINGHGHVASVLGNGS---TNIKGMAPQANLVROSIMDGGL 104
Db 214 QVTASRKNFTSAPTTGIVGHGTAVASIAAGTGAQSRTGYKGVAQGKILNGKVLDAG-- 271
Qy 105 GGLPSNLQTLFSQAYASAGARIHTNSWGAAYNGAYTDSRNVDYTKR--NDMTLIF--AA 160
Db 272 PGDDSGGILAGMEWAQGADIVNMSIG--GMDTETDPLEAUVKLSAEGKILEIAAA 327
Qy 161 GNEGPNGGTISAPGTTAARNATYGTATNLRLPSFGSYADNTTNEVAQFSSRGP-TKDGRGIKPD 219
Db 328 GNEGPQ-SIISPGSDALSATVGA-----VDDDKDIADEFSTGPPGLGDGAVKPD 374
Qy 220 VMAPGTFILSARSSLAPDSSFWANHDSKYAYMGCTSMATPIVAGNAYAQLREHFVKRGIT 279
Db 375 LTAPGVDTIAASAKGNDIAKEVGEKPGYMTISGTSMATPHVAGAAALLKQHPE---- 429
Qy 280 PKPSLIIKAALLAGAAADIGLG-YPNQHNGQGRVTLDSLNLYAYNNESSIS----- 328
Db 430 WRYAERKGALASTKD---GKTYTFPGSGRVQVDIAITQTIVIAEPVSLSGFVQWQPHAD 486
Qy 329 --TSQKATYSFTATGPKLXLSLVSD---APAS--TTASVTLVNDLNLVITAP-NG 377
Db 487 DKPVTKLTYENLGTBDVTLKLSTATGPKSKAAPPGFFTLGASTL-----TVTPANG 538
Qy 378 TQYVGNDFTSPPNDVNGRNNENVENTNAPS---GTYTLEQAVNV 421
Db 539 539 TASVDTYADTRIGGADGTYGSAVYVVTGAGSVRTAAAEFVESTV 586

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Search completed: March 18, 2004, 04:12:40



Qy	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFEQAYS	120	Db	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFEQAYS	120	Qy	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180
Qy	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180	Db	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180	Qy	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180
Qy	121	AGASHTNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180	Db	121	AGASHTNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180	Qy	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240
Qy	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240	Db	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240	Qy	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240
Qy	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240	Db	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240	Qy	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300
Qy	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300	Db	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300	Qy	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300
Qy	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300	Db	241	WAHNDSKYAYMGTTSKATPIVAGNAYQALREHFVNRGTTFKPSLJKALJAGADIGGY	300	Qy	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360
Qy	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360	Db	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360	Qy	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360
Qy	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360	Db	301	PNGNQGGRVTLDKSLNAYNESSLSTSOKATSYSTATGPKLISLWSDAPASTTA	360	Qy	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420
Qy	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420	Db	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420	Qy	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420
Qy	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420	Db	361	SYTLDVNDLVTAPNGTQYGNDFTSPPYNDNDRNNTENVFTNAPQSGTYTIEQAYN	420	Qy	421	VPVGQPTFSLATVN	434
Qy	421	VPVGQPTFSLATVN	434	Db	421	VPVGQPTFSLATVN	434	Qy	421	VPVGQPTFSLATVN	434
Db	421	VPVGQPTFSLATVN	434					RESULT 3			
								US-09-985-689A-2			
								Sequence 2, Application US/09985689A			
								Publication No. USA030022351A1			
								GENERAL INFORMATION:			
								APPLICANT: HATADA, YUJI			
								APPLICANT: OGAWA, AKINORI			
								APPLICANT: KAGEYAMA, YASUISHI			
								APPLICANT: SATO, TSUYOSHI			
								APPLICANT: ARAKI, HIROYUKI			
								APPLICANT: SUMITOMO, NOBUYUKI			
								APPLICANT: OKUDA, MITSUYOSHI			
								APPLICANT: SAEKI, KATSUHIRO			
								APPLICANT: Alkaline protease			
								FILE REFERENCE: 21548US0			
								CURRENT APPLICATION NUMBER: US/09/985,689A			
								CURRENT FILING DATE: 2002-07-01			
								PRIOR APPLICATION NUMBER: JP P2000-355166			
								PRIOR FILING DATE: 2000-11-22			
								PRIOR APPLICATION NUMBER: JP P2001-114048			
								PRIOR FILING DATE: 2001-04-12			
								NUMBER OF SEQ ID NOS: 7			
								SOFTWARE: Patentin version 3.1			
								SEQ ID NO 2			
								LENGTH: 434			
								TYPE: PRT			
								ORGANISM: Bacillus sp.			
								US-09-985-689A-2			
								Query Match	97.5%	Score 2191;	DB 10;
								Best Local Similarity 96.5%;	Pred. No. 6.5e-183;		Gaps 0;
								Matches 419;	Conservative 13;	Mismatches 2;	Indels 0;
								Db	1	NDVARGIVKADVAQSSYGLYQGQIVAVADTGLDTGRNDSSMHEFRGKITALYALGRTN	60
								Qy	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFSQAYS	120
								Db	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFSQAYS	120
								Qy	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180
								Db	121	AGARITHNSWGAIVNGAYTTSRNTDYYRKNDMTILFAAGNEGPNNGTISAPSTAKNAI	180
								Qy	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240
								Db	181	TYGATENLRPSFGSYADNTNEVAQFSSRGPTKDMAPCTFILSARSSLAQDSSF	240
								Qy	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFSQAYS	120
								Db	61	NANDTNGHGHVAGSVLNGSTNGMFAQNLYFQSLMDSGSGLGGPSNQTLFSQAYS	120



14 8 AGARIHTNSWGAAPVNGAYTTDSRNDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 207  
 181 1 TVGATENLRPSFGSYADINNEVAQFSSRGPTKDGRIKPDYMAPGCTFILSARSSAPDSSF 240  
 208 2 TVGATENLRPSFGSYADINNEVAQFSSRGPTKDGRIKPDYMAPGCTFILSARSSAPDSSF 267  
 RESULT 12  
 US-10-090-624-1 ; Sequence 1, Application US/10090624  
 ; Publication No. US20020132335A1 ; GENERAL INFORMATION  
 ; APPLICANT: TAKAKURA, Hikaru ; MORISHITA, Mio  
 ; APPLICANT: SHIMOTO, Tomoko ; APPLICANT: ASADA, Kiyozo  
 ; APPLICANT: KATO, Ikuoshin ; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE  
 ; FILE REFERENCE: TAKAKURA-6  
 ; CURRENT APPLICATION NUMBER: US/1.0/090, 624  
 ; CURRENT FILING DATE: 2002-03-06  
 ; PRIOR APPLICATION NUMBER: 09/445, 472  
 ; PRIOR FILING DATE: 1999-12-06  
 ; PRIOR APPLICATION NUMBER: 151969/1997  
 ; PRIOR FILING DATE: 1997-06-10  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 412  
 ; TYPE: PRT ; ORGANISM: Pyrococcus furiosus  
 US-10-090-624-1 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 18 GLYQQQIVAVADTGILDGRNDSSMHEFRGKITALYALGRTNNAN-----DTNGHGT 71  
 Db 22 GVDGSGITIGIDGTGID-----ASFDLQGKV-----IGWVDFYNGRSVPYDDGHHGT 70  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 72 VAGSVLNGSTN-----KGMAPQANLYEQSTIM-----DSGGGLGGLPSNQTLFSQASAGARI 125  
 Db 71 VASIAAGTGAASNGKKGMAPAKLGIKVADGGSISISTIKGVEWAVDNKDKYGIKV 130  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 126 HTNSWGA-----AVNGAYTTDSRNDDYRKNDMTILFAAGNEGPGSGTISAP 173  
 Db 131 INFISLGSSQSSDGTALSQAVNAWDA-----GIVVVAAGNSPNKTYTIGSP 178  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 174 GPKNAITYVGATENLRPSFGSYADINNHVAQFSSRGPTKDGRIKPDYMAPGCTFILSARSS 233  
 Db 179 AAASKVTVGA-----VDKCDVITFSRSPATDGRKLKPVAVPNWIIARAS 227  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 234 LADPSFWANHDSKAYAUNGTSMATPVAGNAQLEBFVKNRGTPK-----PSLLKALIA 291  
 Db 228 -----GTSMQOPTNDYTTAAPGTSMATPVAVTAUJLQ-----APSWTIDKVVKALIE 277  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 292 GA-----ADIGLYGPNGNGWGVTLDSKLNAYVNESSLSLSQKA-----TYSFT 338  
 Db 278 TADIVKDEIADIAYGK-----GRVNAKAIN-YDNYAKLUVFGVYVANKGSQTHQFV 328  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 339 ATAGKPKLISLYWSDAPASTTASVTLVNDLIVITAPNGTQYVGNDFTSPPNDMIDGRNN 398  
 Db 329 ISGASFVTTATLWDNAN-----SDDLILYDPNGNQ-VDYSYTAY-----G 369  
 ; Query Match 18.4%; Score 414; DB 13; Length 412;  
 Best Local Similarity 29.8%; Pred. No. 1.5e-27; Matches 136; Mismatches 147; Indels 114; Gaps 19;  
 Qy 399 VENVYNAFQSGPYTEVQAYNVPGEQQTFSLAIN 434  
 Db 370 FERKGYNPTDGTWIKVSVS-----GSANYQDVVS 402  
 ; GENERAL INFORMATION:  
 RESULT 13  
 US-10-090-624-4 ; Sequence 4, Application US/10090624  
 ; Publication No. US20020132335A1 ; GENERAL INFORMATION:

FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
 PRIORITY FILING DATE: 1999-12-06  
 PRIORITY APPLICATION NUMBER: US/10/090,624  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 1999-12-06  
 PRIORITY NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 4  
 LENGTH: 522  
 TYPE: PRT  
 ORGANISM: Pyrococcus furiosus  
 FEATURE: misc feature  
 NAME/KEY: misc feature  
 LOCATION: (428)..(428)  
 OTHER INFORMATION: Xaa at position 428 is Gly or Val.

Query Match 18.4%; Score 414; DB 13; Length 654;  
 Best Local Similarity 29.8%; Prod. No. 2.9e-27;  
 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 SEQ ID NO 16  
 US-10-090-624-16

Query Match 18.4%; Score 414; DB 13; Length 654;  
 Best Local Similarity 29.8%; Prod. No. 2.9e-27;  
 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 72 VAGSVLGNGSTN----KGMAPQANLVFQSMNLTLSQYASAGARI 125  
 Db 203 VASIAAGTGAASNGKYKGAPAKLAGIKVLAGDSGTSISTIKGVETAVDNKDKYGIKV 262  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 263 INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTGSP 310  
 Qy 174 GTAKNAITVGATENLRPSGSYADNNHVAQFSSRGPTKDGRKIPDMPGTFILSARS 233  
 Db 311 AAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 359  
 Qy 71 VASIAAGTGAASNGKYKGAPAKLAGIKVLAGDSGSSSTIKGVETAVDNKDKYGIKV 130  
 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 131. INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTIGSP 178  
 Qy 234 LAPDSSFWANHDSKYAAYNGGTSMATPIVAGNVAQLREHFVNRGTPK--PSLKKALIA 291  
 Db 360 --GTSMGQPINDDYTTAAGTSMWATPHYGAALLQ-----AHPSWTPDKVKTALIE 409  
 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
 Qy 339 ATAGKPLKISLWSDAPASTTASVTLVNDLVTAPNGTQVGNDFTSYNDNWGRNN 398  
 Db 461 ISGASFVTATLYWDNAN-----SDLDLYDPMQNGQ--VDTSYTAYY----G 501  
 Qy 399 VENYFINAPQSGETTIEVQAYNVEPGPQTSLAINV 434  
 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
 US-10-112-488-39  
 Sequence 39. Application US/10112488  
 Publication No. US20030082746A1  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: 219216US00CNT  
 CURRENT APPLICATION NUMBER: US/10/112,488  
 CURRENT FILING DATE: 2002-04-01  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
 PRIORITY FILING DATE: 1999-12-06  
 PRIORITY APPLICATION NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 16

Query Match 18.4%; Score 414; DB 13; Length 654;  
 Best Local Similarity 29.8%; Prod. No. 2.9e-27;  
 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 263 INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTGSP 310  
 Qy 174 GTAKNAITVGATENLRPSGSYADNNHVAQFSSRGPTKDGRKIPDMPGTFILSARS 233  
 Db 311 AAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 359  
 Qy 71 VASIAAGTGAASNGKYKGAPAKLAGIKVLAGDSGSSSTIKGVETAVDNKDKYGIKV 130  
 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 131. INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTIGSP 178  
 Qy 234 LAPDSSFWANHDSKYAAYNGGTSMATPIVAGNVAQLREHFVNRGTPK--PSLKKALIA 291  
 Db 360 --GTSMGQPINDDYTTAAGTSMWATPHYGAALLQ-----AHPSWTPDKVKTALIE 409  
 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
 Qy 339 ATAGKPLKISLWSDAPASTTASVTLVNDLVTAPNGTQVGNDFTSYNDNWGRNN 398  
 Db 461 ISGASFVTATLYWDNAN-----SDLDLYDPMQNGQ--VDTSYTAYY----G 501  
 Qy 399 VENYFINAPQSGETTIEVQAYNVEPGPQTSLAINV 434  
 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
 US-10-112-488-39  
 Sequence 39. Application US/10112488  
 Publication No. US20030082746A1  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: 219216US00CNT  
 CURRENT APPLICATION NUMBER: US/10/112,488  
 CURRENT FILING DATE: 2002-04-01  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
 PRIORITY FILING DATE: 1999-12-06  
 PRIORITY APPLICATION NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 16

Query Match 18.4%; Score 414; DB 13; Length 654;  
 Best Local Similarity 29.8%; Prod. No. 2.9e-27;  
 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 263 INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTGSP 310  
 Qy 174 GTAKNAITVGATENLRPSGSYADNNHVAQFSSRGPTKDGRKIPDMPGTFILSARS 233  
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 Qy 71 VASIAAGTGAASNGKYKGAPAKLAGIKVLAGDSGSSSTIKGVETAVDNKDKYGIKV 130  
 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 131. INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTIGSP 178  
 Qy 234 LAPDSSFWANHDSKYAAYNGGTSMATPIVAGNVAQLREHFVNRGTPK--PSLKKALIA 291  
 Db 360 --GTSMGQPINDDYTTAAGTSMWATPHYGAALLQ-----AHPSWTPDKVKTALIE 409  
 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
 Qy 339 ATAGKPLKISLWSDAPASTTASVTLVNDLVTAPNGTQVGNDFTSYNDNWGRNN 398  
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 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
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 Sequence 39. Application US/10112488  
 Publication No. US20030082746A1  
 PRIORITY NUMBER: PCT/JP00/06780  
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 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
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 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: 219216US00CNT  
 CURRENT APPLICATION NUMBER: US/10/112,488  
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 PRIORITY NUMBER: PCT/JP00/06780  
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 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
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Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 263 INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTGSP 310  
 Qy 174 GTAKNAITVGATENLRPSGSYADNNHVAQFSSRGPTKDGRKIPDMPGTFILSARS 233  
 Db 311 AAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 359  
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 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
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 Db 360 --GTSMGQPINDDYTTAAGTSMWATPHYGAALLQ-----AHPSWTPDKVKTALIE 409  
 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
 Qy 339 ATAGKPLKISLWSDAPASTTASVTLVNDLVTAPNGTQVGNDFTSYNDNWGRNN 398  
 Db 461 ISGASFVTATLYWDNAN-----SDLDLYDPMQNGQ--VDTSYTAYY----G 501  
 Qy 399 VENYFINAPQSGETTIEVQAYNVEPGPQTSLAINV 434  
 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
 US-10-112-488-39  
 Sequence 39. Application US/10112488  
 Publication No. US20030082746A1  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
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FILE REFERENCE: 219216US00CNT  
 CURRENT APPLICATION NUMBER: US/10/112,488  
 CURRENT FILING DATE: 2002-04-01  
 PRIORITY NUMBER: PCT/JP00/06780  
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 PRIORITY APPLICATION NUMBER: JP2000-280098  
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 PRIORITY APPLICATION NUMBER: JP11-280098  
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 NUMBER OF SEQ ID NOS: 70

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 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
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 PRIORITY APPLICATION NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
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 SEQ ID NO 16

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 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
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 Db 311 AAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 359  
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 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 131. INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTIGSP 178  
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 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
 Qy 339 ATAGKPLKISLWSDAPASTTASVTLVNDLVTAPNGTQVGNDFTSYNDNWGRNN 398  
 Db 461 ISGASFVTATLYWDNAN-----SDLDLYDPMQNGQ--VDTSYTAYY----G 501  
 Qy 399 VENYFINAPQSGETTIEVQAYNVEPGPQTSLAINV 434  
 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
 US-10-112-488-39  
 Sequence 39. Application US/10112488  
 Publication No. US20030082746A1  
 PRIORITY NUMBER: PCT/JP00/06780  
 PRIORITY FILING DATE: 2000-09-29  
 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: 219216US00CNT  
 CURRENT APPLICATION NUMBER: US/10/112,488  
 CURRENT FILING DATE: 2002-04-01  
 PRIORITY NUMBER: PCT/JP00/06780  
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 PRIORITY APPLICATION NUMBER: JP2000-280098  
 PRIORITY FILING DATE: 2000-06-28  
 PRIORITY APPLICATION NUMBER: JP11-280098  
 PRIORITY FILING DATE: 1999-09-30  
 NUMBER OF SEQ ID NOS: 70

FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-06  
 PRIORITY NUMBER: 1999-12-06  
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 PRIORITY APPLICATION NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 16

Query Match 18.4%; Score 414; DB 13; Length 654;  
 Best Local Similarity 29.8%; Prod. No. 2.9e-27;  
 Matches 136; Conservative 59; Mismatches 147; Gaps 19;

Qy 18 GLYGGQIVAVADTGLDTGRNDSSMHEAFRKITALYALGRITNNAN----DTNGHGTTH 71  
 Db 154 GYDGGITGIGIDGID----ASHPDQLQKV----IGWVDFNGRSYPDDHGHTH 202  
 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 263 INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTGSP 310  
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 Db 311 AAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 359  
 Qy 71 VASIAAGTGAASNGKYKGAPAKLAGIKVLAGDSGSSSTIKGVETAVDNKDKYGIKV 130  
 Db 126 HTNSWGA-----AVNGAYTDSRNVDYRNDMFTLFAAGNEGPGNGTISAP 173  
 Db 131. INLSGSSQSSDGTDALSAVNANWDA-----GLVvvVAAGNSGPKYTIGSP 178  
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 Db 360 --GTSMGQPINDDYTTAAGTSMWATPHYGAALLQ-----AHPSWTPDKVKTALIE 409  
 Qy 292 GA-----ADIGVYPNQNGWGRVTLDSKUNVAYNNESSSLSTSOKA----TYSFT 338  
 Db 410 TADIVKPDFAIDIAYGA-----GRVNAKYAIN--IDNYAKLUVFTGYVANKGSCTRQFV 460  
 Db 179 AAAASKVITYGA-----VTDKYDVTFSRSGPTADGRKIPVAPGNWIIARAS 227  
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 Db 502 FERKVYNTPDGTMWIKVVSYS--GSANYQVDVVS 534

RESULT 15  
 US-10-090-624-16  
 Sequence 16. Application US/10090624  
 GENERAL INFORMATION:  
 APPLICANT: TAKAKURA, Hikaru  
 APPLICANT: MORISHITA, Mio  
 APPLICANT: SHIMOJO, Tomoko  
 APPLICANT: ASADA, Kiyozu  
 TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Streptomyces albogriseolus
US-10-112-488-39

Query Match 16.3% Score 366; DB 14; Length 1079;
Best Local Similarity 31.6% Prod. No. 9.4e-23; Length 1079;
Matches 148; Conservative 55; Mismatches 15; Indels 90; Gaps 20;
Db 160 VARYWLDGVRKASLDTSQGIGTPKAWAEAGYDGRGVKIAVLDTGVD-----ATHDLKG 213

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Db 160 VARYWLDGVRKASLDTSQGIGTPKAWAEAGYDGRGVKIAVLDTGVD-----ATHDLKG 213

QY 49 KITALYALGRTNNANDTIGHGTHAVGSLVNGS----TINKGNAPOANLYFQSIMDSGGGL 104
Db 214 QVTAASKNFTSAAPTGDDVYGHGTHAVIAAGTGRQSKGTYKGVAPGAKILNGVYLDAG-- 271

QY 105 GGLESNLQTFLFSQAYSAGARIAHTNSWGAIVNGAYTDSRNVDYVRK--NDMTILE--AA 160
Db 272 FGDDSGILAGMEEAAAGDIVNMSLG----GNDTPEDPLERAVDKLSAERGLPAA 327

QY 161 GNEGNGGTISAPGTAKNATIVGATENRPSFSYADMINHYAQFSSRGP-TKDGRKPD 219
Db 328 GNEGFP- -SIGSPSSADSLTGR-----VDEDKLADFSSTGPRLGDAVKPD 374

QY 220 VMAPOTFLISARSSAAPPFWANHDSKTYAYMGETSMATPIAVGNAQLREFVRNQGIT 279
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QY 280 PKPSLILKAALIAGAADIGLIG-YPNNGNOMGRVTLDKSLNVAYNESSSL----- 328
QY 430 WRYABLKGAITASTKD--GKYPPEFQQSGRVQUDKAQTQVIAEPVLSFGVQQNPHAD 486
Db 329 ---TSQKATYTSFTATAKPIKISLWSD----APAS---TTASVTLVNDLVLITAP-NG 377
QY 487 DKPVTKKLTYRNLTGDTVTLKLSTATGKRAAPAGFFLGASTL-----TVPANG 538

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Db 539 TASVDTAIDTRLGGAVDGTYSAYVATGAGQSVRTAAAVEREVESYNN 586

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Search completed: March 18, 2004, 04:11:41  
 Job time : 46 secs